FIGURE 1

```
Eciss   ATGCAGGATAATAAGATGAAAAAAATGTTATTTTCTGCCGCTCTGGCAATGCTTATTACA   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
102iss  ATGCAGGATAATAAGATGAAAAAAATGTTATTTTCTGCCGCTCTGGCAATGCTTATTACA   60
        |  ||||  |  ||||||||||||  ||  |  ||  |  ||  |||||  ||||||||||
lambor  ATCGGGAATAACACCATGAAAAAAATGCTACTCGCTACTGCGCTGGCCCTGCTTATTACA   60

Eciss   GGATGTGCTCAACAAACGTTTACTGTTGGAAACAAACCGACAGCAGTAACACCAAAGGAA   120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
102iss  GGATGTGCTCAACAAACGTTTACTGTTGGAAACAAACCGACAGCAGTAACACCAAAGGAA   120
        ||||||||||||||  ||||||||||||  ||||||||||  ||||||||  ||||||||||
lambor  GGATGTGCTCAACAGACGTTTACTGTTCAAAACAAACCGGCAGCAGTAGCACCAAAGGAA   120

Eciss   ACCATCACTCATCATTTCTTCGTTTCCCCAATTGGAC-AGAGAAAACTGTTGATGCAGCC   179
        ||||||||||||||||||||||||||  ||||||||  ||||||||||||||||||||||
102iss  ACCATCACTCATCATTTCTTCGTTTCGGGAATTGGACAAGAGAAAACTGTTGATGCAGCC   180
        ||||||||  ||||||||||||||||  ||||||||  ||  ||||||||||  |||||||||
lambor  ACCATCACCCATCATTTCTTCGTTTCTGGAATTGGGCAGAAGAAAACTGTCGATGCAGCC   180

Eciss   AAAATTTGTTGGCGGTGCAGAAAATGTTGTTAAAACAGAAACTCAGCAAACATTCGTAAA   239
        ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
102iss  AAAATTTG-TGGCGGTGCAGAAAATGTTGTTAAAACAGAAACTCAGCAAACATTCGTAAA   239
        ||||||||  ||||||  ||||||||||||||||||||||||  ||||||||||||||||||
lambor  AAAATTTG-TGGCGGCGCAGAAAATGTTGTTAAAACAGAAACCCAGCAAACATTCGTAAA   239

Eciss   TGCATTGCCCGGTTTTATCACTTTTGGCATCTATACTCCGCGGGAAACCCGTGTATATTG   299
        ||  |||||  ||||||||||||||||||||||||||||||  ||||  ||||  ||||||||
102iss  TGGATTGCTCGGTTTTATCACTTTTGGCATCTATACTCCGCTGGAAGCCCGGGTATATTG   299
        ||||||||||||||||  |||||  |||||  ||||||||||||||||  ||  ||  |||||
lambor  TGGATTGCTCGGTTTTATTACTTTAGGCATTTATACTCCGCTGGAAGCGCGTGTGTATTG   299

Eciss   CTCACAATAG                                                     309
        ||||||||||
102iss  CTCACAATAG                                                     309
        |||||||||
lambor  CTCACAATAA                                                     309
```

FIGURE 2

```
Iss_Ec MQDNKMKKMLFSAALAMLITGCAQQTFTVGNKPTAVTPKETITHHFFVSPIGQRKLLMQP  60
       ||||||||||||||||||||||||||||||||||||||:||||||||| ||| | : ::
102Iss MQDNKMKKMLFSAALAMLITGCAQQTFTVGNKPTAVTPKETITHHFFVSGIGQEKTVDAA  60
       |||||:::|||:|||||||||||| |||:||:||:|||||||||||||:||||||
lamBor      MKKMLLATALALLITGCAQQTFTVQNKPAAVAPKETITHHFFVSGIGQKKTVDAA  55

Iss_Ec KFVGGAENVVKTETQQTFVNALPGFITFGIYTPRETRVYCSQ                  102
       |: ||||||||||||||||||:| |||||||||| |:||||||
102Iss KICGGAENVVKTETQQTFVNGLLGFITFGIYTPLEARVYCSQ                  102
       ||||||||||||||||||||||||||:|||||||||||||||
lamBor KICGGAENVVKTETQQTFVNGLLGFITLGIYTPLEARVYCSQ                  97
```

FIGURE 3

```
 L   E   V   L   F   Q   G   P   L   G   S   M   Q   D   N
CTG GAA GTT CTG TTC CAG GGG CCC CTG GGA TCC ATG CAG GAT AAT
PreScission Protease                BamHI  iss fusion start

 K   M   K   K   M   L   F   S   A   A   L   A   M   L   I
AAG ATG AAA AAA ATG TTA TTT TCT GCC GCT CTG GCA ATG CTT ATT

 T   G   C   A   Q   Q   T   F   T   V   G   N   K   P   T
ACA GGA TGT GCT CAA CAA ACG TTT ACT GTT GGA AAC AAA CCG ACA

 A   V   T   P   K   E   T   I   T   H   H   F   F   V   S
GCA GTA ACA CCA AAG GAA ACC ATC ACT CAT CAT TTC TTC GTT TCG

 G   I   G   Q   E   K   T   V   D   A   A   K   I   C   G
GGA ATT GGA CAA GAG AAA ACT GTT GAT GCA GCC AAA ATT TGT GGC

 G   A   E   N   V   V   K   T   E   T   Q   Q   T   F   V
GGT GCA GAA AAT GTT GTT AAA ACA GAA ACT CAG CAA ACA TTC GTA

 N   G   L   L   G   F   I   T   F   G   I   Y   T   P   L
AAT GGA TTG CTC GGT TTT ATC ACT TTT GGC ATC TAT ACT CCG CTG

 E   A   R   V   Y   C   S   Q   *
GAA GCC CGG GTA TAT TGC TCA CAA TAG TTG CCC ATC GAT ATG GGG

AGC TCA TCT GCG AAT TCC
          EcoRI
```

FIGURE 4

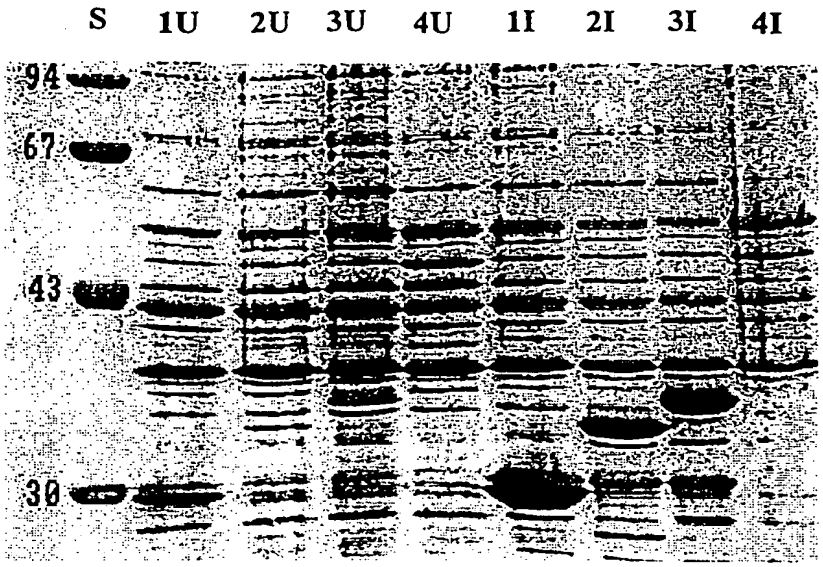
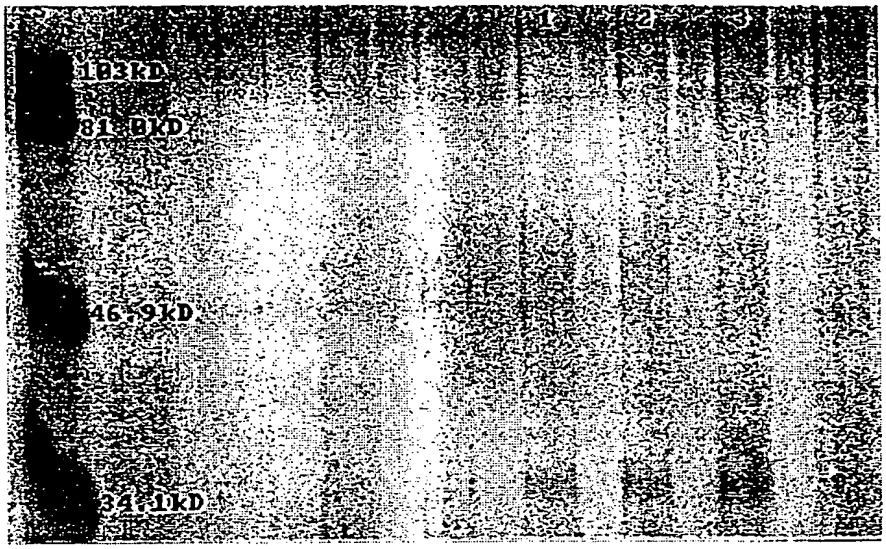


FIGURE 5



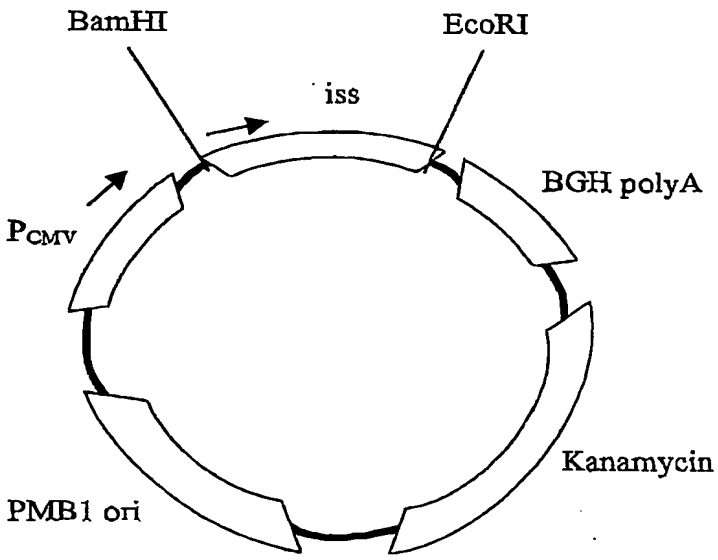


Fig 6